

SEQUENCE LISTING

<110> Nicolaides, Nicholas
 Grasso, Luigi
 Sass, Philip
 Kinzler, Kenneth
 Vogelstein, Bert

<120> A method for generating hypermutable
 plants

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 Ser Ser Ser Ile Ser Val Val Lys Asp Gly Gly Leu Lys Leu Ile
 65 70 75 80
 Gln Val Ser Asp Asp Gly His Gly Ile Arg Arg Glu Asp Leu Pro Ile
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 Leu Cys Glu Arg His Thr Thr Ser Lys Leu Thr Lys Phe Glu Asp Leu
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 115 120 125
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 His Gly Tyr Arg Val Ser Tyr Arg Asp Gly Val Met Glu His Glu Pro
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 Val His Ser Val Val Ser Pro Ser Arg Leu Asp Ser Ile Arg Ser Val
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 Cys Asp Ser Ser Gly Cys Thr Phe Asp Met Glu Gly Phe Ile Ser Asn
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 Tyr Val Gly Met Ala Asp Asp Val Phe Ala Leu Val Gln Tyr Asn Thr
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 Leu Ser Leu Ser Thr Ala Val Lys Glu Leu Val Glu Asn Ser Leu Asp
 35 40 45
 Ala Gly Ala Thr Asn Ile Asp Leu Lys Leu Lys Asp Tyr Gly Val Asp
 50 55 60
 Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe
 65 70 75 80
 Glu Gly Leu Thr Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala
 85 90 95
 Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser
 100 105 110
 Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Ala Ser
 115 120 125
 Ala Lys Val Gly Thr Arg Leu Met Phe Asp His Asn Gly Lys Ile Ile
 130 135 140
 Gln Lys Thr Pro Tyr Pro Arg Pro Arg Gly Thr Thr Val Ser Val Gln
 145 150 155 160
 Gln Leu Phe Ser Thr Leu Pro Val Arg His Lys Glu Phe Gln Arg Asn
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 Ile Lys Lys Glu Tyr Ala Lys Met Val Gln Val Leu His Ala Tyr Cys
 180 185 190
 Ile Ile Ser Ala Gly Ile Arg Val Ser Cys Thr Asn Gln Leu Gly Gln
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 Gly Lys Arg Gln Pro Val Val Cys Thr Gly Gly Ser Pro Ser Ile Lys
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 Glu Asn Ile Gly Ser Val Phe Gly Gln Lys Gln Leu Gln Ser Leu Ile
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 Pro Phe Val Gln Leu Pro Pro Ser Asp Ser Val Cys Glu Glu Tyr Gly
 245 250 255
 Leu Ser Cys Ser Asp Ala Leu His Asn Leu Phe Tyr Ile Ser Gly Phe
 260 265 270
 Ile Ser Gln Cys Thr His Gly Val Gly Arg Ser Ser Thr Asp Arg Gln
 275 280 285
 Phe Phe Phe Ile Asn Arg Arg Pro Cys Asp Pro Ala Lys Val Cys Arg
 290 295 300
 Leu Val Asn Glu Val Tyr His Met Tyr Asn Arg His Gln Tyr Pro Phe
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 Val Val Leu Asn Ile Ser Val Asp Ser Glu Cys Val Asp Ile Asn Val
 325 330 335
 Thr Pro Asp Lys Arg Gln Ile Leu Leu Gln Glu Glu Lys Leu Leu Leu
 340 345 350
 Ala Val Leu Lys Thr Ser Leu Ile Gly Met Phe Asp Ser Asp Val Asn
 355 360 365
 Lys Leu Asn Val Ser Gln Gln Pro Leu Leu Asp Val Glu Gly Asn Leu
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 Ile Lys Met His Ala Ala Asp Leu Glu Lys Pro Met Val Glu Lys Gln
 385 390 395 400
 Asp Gln Ser Pro Ser Leu Arg Thr Gly Glu Glu Lys Lys Asp Val Ser
 405 410 415
 Ile Ser Arg Leu Arg Glu Ala Phe Ser Leu Arg His Thr Thr Glu Asn
 420 425 430
 Lys Pro His Ser Pro Lys Thr Pro Glu Pro Arg Arg Ser Pro Leu Gly
 435 440 445
 Gln Lys Arg Gly Met Leu Ser Ser Ser Thr Ser Gly Ala Ile Ser Asp
 450 455 460
 Lys Gly Val Leu Arg Pro Gln Lys Glu Ala Val Ser Ser Ser His Gly
 465 470 475 480
 Pro Ser Asp Pro Thr Asp Arg Ala Glu Val Glu Lys Asp Ser Gly His
 485 490 495
 Gly Ser Thr Ser Val Asp Ser Glu Gly Phe Ser Ile Pro Asp Thr Gly
 500 505 510
 Ser His Cys Ser Ser Glu Tyr Ala Ala Ser Ser Pro Gly Asp Arg Gly

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Ser Phe Ser Asp Val Asp	Cys His Ser Asn Gln	Glu Asp Thr Gly Cys
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Lys Phe Arg Val Leu Pro	Gln Pro Thr Asn Leu Ala	Thr Pro Asn Thr
565	570	575
Lys Arg Phe Lys Lys Glu	Glu Ile Leu Ser Ser Asp	Ile Cys Gln
580	585	590
Lys Leu Val Asn Thr Gln	Asp Met Ser Ala Ser Gln	Val Asp Val Ala
595	600	605
Val Lys Ile Asn Lys Lys	Val Val Pro Leu Asp	Phe Ser Met Ser Ser
610	615	620
Leu Ala Lys Arg Ile Lys	Gln Leu His His	Glu Ala Gln Gln Ser
625	630	635
Gly Glu Gln Asn Tyr Arg	Lys Phe Arg Ala Lys	Ile Cys Pro Gly Glu
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Asn Gln Ala Ala Glu Asp	Glu Leu Arg Lys Glu	Ile Ser Lys Thr Met
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Phe Ala Glu Met Glu Ile Ile	Gly Gln Phe Asn Leu	Gly Phe Ile Ile
675	680	685
Thr Lys Leu Asn Glu Asp	Ile Phe Ile Val Asp	Gln His Ala Thr Asp
690	695	700
Glu Lys Tyr Asn Phe Glu	Met Leu Gln Gln	His Thr Val Leu Gln
705	710	715
Gln Arg Leu Ile Ala Pro	Gln Thr Leu Asn Leu	Thr Ala Val Asn Glu
725	730	735
Ala Val Leu Ile Glu Asn	Leu Glu Ile Phe Arg	Lys Asn Gly Phe Asp
740	745	750
Phe Val Ile Asp Glu Asn	Ala Pro Val Thr Glu	Arg Ala Lys Leu Ile
755	760	765
Ser Leu Pro Thr Ser Lys	Asn Trp Thr Phe Gly	Pro Gln Asp Val Asp
770	775	780
Glu Leu Ile Phe Met Leu	Ser Asp Ser Pro Gly	Val Met Cys Arg Pro
785	790	795
Ser Arg Val Lys Gln Met	Phe Ala Ser Arg Ala	Cys Arg Lys Ser Val
805	810	815
Met Ile Gly Thr Ala Leu	Asn Thr Ser Glu Met	Lys Lys Leu Ile Thr
820	825	830
His Met Gly Glu Met Asp	His Pro Trp Asn Cys	Pro His Gly Arg Pro
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Val	Ile	Leu	Asp	Leu	Ser	Ser	Ala	Val	Lys	Glu	Leu	Val	Glu	Asn	Ser
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Glu	Asp	Tyr	Phe	Gln	Val	Ile	Asp	Asn	Gly	Cys	Gly	Ile	Ser	Pro	Thr
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Ala	Leu	Lys	His	His	Thr	Ser	Lys	Leu	Glu	Asp	Phe	Thr	Asp	Leu	Leu

Asn	Leu	Thr	Thr	Tyr	Gly	Phe	Arg	Gly	Glu	Ala	Leu	Ser	Ser	Leu	Cys
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Ala	Leu	Gly	Asn	Leu	Thr	Val	Glu	Thr	Arg	Thr	Lys	Asn	Glu	Pro	Val
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Ala	Thr	Leu	Leu	Thr	Phe	Asp	His	Ser	Gly	Leu	Leu	Thr	Ala	Glu	Lys
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Lys	Thr	Ala	Arg	Gln	Ile	Gly	Thr	Thr	Val	Thr	Val	Arg	Lys	Leu	Phe
	165								170						175
Ser	Asn	Leu	Pro	Val	Arg	Ser	Lys	Glu	Phe	Lys	Arg	Asn	Ile	Arg	Lys
	180						185						190		
Glu	Tyr	Gly	Lys	Leu	Val	Ser	Leu	Leu	Asn	Ala	Tyr	Ala	Leu	Ile	Ala
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Lys	Gly	Val	Arg	Phe	Val	Cys	Ser	Asn	Thr	Thr	Gly	Lys	Asn	Pro	Lys
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Ser	Val	Val	Leu	Asn	Thr	Gln	Gly	Arg	Gly	Ser	Leu	Lys	Asp	Asn	Ile
	225				230				235						240
Ile	Thr	Val	Phe	Gly	Ile	Ser	Thr	Phe	Thr	Ser	Leu	Gln	Pro	Gly	Thr
	245							250				255			
Gly	Arg	Asn	Leu	Ala	Asp	Arg	Gln	Tyr	Phe	Phe	Ile	Asn	Gly	Arg	Pro
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Val	Asp	Met	Pro	Lys	Val	Ser	Lys	Leu	Val	Asn	Glu	Leu	Tyr	Lys	Asp
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Thr	Ser	Ser	Arg	Lys	Tyr	Pro	Val	Thr	Ile	Leu	Asp	Phe	Ile	Val	Pro
												290	295	300	
Gly	Gly	Ala	Cys	Asp	Leu	Asn	Val	Thr	Pro	Asp	Lys	Arg	Lys	Val	Phe
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Phe	Ser	Asp	Glu	Thr	Ser	Val	Ile	Gly	Ser	Leu	Arg	Glu	Gly	Leu	Asn
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Glu	Ile	Tyr	Ser	Ser	Asn	Ala	Ser	Tyr	Ile	Val	Asn	Arg	Phe	Glu	
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Lys	Ser	Asn	Leu	Leu	Ser	Glu	Gly	Ile	Val	Leu	Asp	Val	Ser	Ser	Lys
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Val	Glu	Ile	Asp	Asn	Ser	Ser	Pro	Met	Glu	Lys	Phe	Lys	Phe	Glu	Ile
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Val	Thr	Glu	Lys	Val	Thr	Asp	Ala	Ser	Lys	Asp	Leu	Ser	Ser	Arg	Ser
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Glu	Arg	Asp	Leu	Phe	Ile	Val	Asp	Gln	His	Ala	Ala	Asp	Glu	Lys	Phe
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Asn	Phe	Glu	His	Leu	Ala	Arg	Ser	Thr	Val	Leu	Asn	Gln	Gln	Pro	Leu
											595	600	605		

Leu Gln Pro Leu Asn Leu Glu Leu Ser Pro Glu Glu Glu Val Thr Val
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 Leu Met His Met Asp Ile Ile Arg Glu Asn Gly Phe Leu Leu Glu Glu
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 Asn Pro Ser Ala Pro Pro Gly Lys His Phe Arg Leu Arg Ala Ile Pro
 645 650 655
 Tyr Ser Lys Asn Ile Thr Phe Gly Val Glu Asp Leu Lys Asp Leu Ile
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 Ser Thr Leu Gly Asp Asn His Gly Glu Cys Ser Val Ala Ser Ser Tyr
 675 680 685
 Lys Thr Ser Lys Thr Asp Ser Ile Cys Pro Ser Arg Val Arg Ala Met
 690 695 700
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 Arg Lys Asn Glu Met Gln Lys Ile Val Glu His Leu Ala Asp Leu Glu
 725 730 735
 Ser Pro Trp Asn Cys Pro His Gly Arg Pro Thr Met Arg His Leu Val
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 Ala Gly Ala Thr Asn Ile Asp Leu Lys Leu Lys Asp Tyr Gly Val Asp
 50 55 60
 Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Asn Phe
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 Glu Gly Leu Thr Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala
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 Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser
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 Glu Asp Tyr Phe Gln Val Ile Asp Asn Gly Cys Gly Ile Ser Pro Thr

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Asn Phe Lys Val Cys Val Gln Ile Leu Arg Arg Thr Phe Asp Val Leu
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Ala Leu Lys His His Thr Ser Lys Leu Glu Asp Phe Thr Asp Leu Leu
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Asn Leu Thr Thr Tyr Gly Phe Arg Gly Glu Ala Leu Ser Ser Leu Cys
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Ala Leu Gly Asn Leu Thr Val Glu Thr Arg Thr Lys Asn Glu Pro Val
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Ala Thr Leu
145

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	GAG	TTA	GTA	GAA	AAC	AGT	CTG	GAT	GCT	GGT	GCC	ACT	AAT	ATT	GAT	CTA	AAG	CTT	AAG	GAC	
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1201	D	Q	S	P	S	L	R	T	G	E	E	K	K	D	V	S	I	S	R	L	
	GAT	CAA	TCC	CCT	TCA	TTA	AGG	ACT	GGA	GAA	GAA	AAA	AAA	GAC	GTC	TCC	ATT	TCC	AGA	CTG	
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1441	P	S	D	P	T	D	R	A	E	V	E	K	D	S	G	H	G	S	T	S	
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1621	E	T	D	D	S	F	S	D	V	C	H	S	N	Q	E	D	T	G	C		
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1981	E	D	E	L	R	K	E	I	S	K	T	M	F	A	E	M	E	I	I	G	
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2101	H	A	T	D	E	K	Y	N	F	E	M	L	Q	Q	H	T	V	L	Q	G	
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2161	Q	R	L	I	A	P	Q	T	L	N	L	T	A	V	N	E	A	V	L	I	
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2221	E	N	L	E	I	F	R	K	N	G	F	D	F	V	I	D	E	N	A	P	
	GAA	AAT	CTG	GAA	ATA	TTT	AGA	AAG	AA	GGC	TTT	GAT	TTT	GTT	ATC	GAT	GAA	AAT	GCT	CCA	

V T E R A K L I S L P T S K N W T F G P
2281 GTC ACT GAA AGG GCT AAA CTG ATT TCC TTG CCA ACT AGT AAA AAC TGG ACC TTC GGA CCC
Q D V D E L I F M L S D S P G V M C R P
2341 CAG GAC GTC GAT GAA CTG ATC TTC ATG CTG AGC GAC AGC CCT GGG GTC ATG TGC CGG CCT
S R V K Q M F A S R A C R K S V M I G T
2401 TCC CGA GTC AAG CAG ATG TTT GCC TCC AGA GCC TGC CGG AAG TCG GTG ATG ATT CGG ACT
A L N T S E M K K L I T H M G E M D H P
2461 GCT CTT AAC ACA AGC GAG ATG AAG AAA CTG ATC ACC CAC ATG GGG GAG ATG GAC CAC CCC
W N C P H G R P T M R H I A N L G V I S
2521 TGG AAC TGT CCC CAT GGA AGG CCA ACC ATG AGA CAC ATC GCC AAC CTG GGT GTC ATT TCT
Q N *
2581 CAG AAC TAG

Sequence ID 3. Human PMS2 (ACCESSION U13696) cDNA and amino acid sequences.

bio2text v1.2.0

	M	Q	G	D	S	S	P	S	P	T	T	T	S	S	P	L	I	R	P	I	
1	ATG	CAA	GGA	GAT	TCT	TCT	CCG	TCT	CCG	ACG	ACT	ACT	AGC	TCT	CCT	TTG	ATA	AGA	CCT	ATA	
	N	R	N	V	I	H	R	I	C	S	G	Q	V	I	L	D	L	S	S	A	
61	AAC	AGA	AAC	GTA	ATT	CAC	AGA	ATC	TGT	TCC	GGT	CAA	GTC	ATC	TTA	GAC	CTC	TCT	TCG	GCC	
	V	K	E	L	V	E	N	S	L	D	A	G	A	T	S	I	E	I	N	L	
121	GTC	AAG	GAG	CTT	GTC	GAG	AAT	AGT	CTC	GAC	GCC	GGC	GCC	ACC	AGT	ATA	GAG	ATT	AAC	CTC	
	R	D	Y	G	E	D	Y	F	Q	V	I	D	N	G	C	G	I	S	P	T	
181	CGA	GAC	TAC	GCG	GAA	GAC	TAT	TTT	CAG	GTC	ATT	GAC	AAT	GGT	TGT	GGC	ATT	TCC	CCA	ACC	
	N	F	K	V	C	V	Q	I	L	R	R	T	F	D	V	L	A	L	K	H	
241	AAT	TTC	AAG	GTT	TGT	GTC	CAA	ATT	CTC	CGA	AGA	ACT	TTT	GAT	TTT	CTT	GCA	CTT	AAG	CAT	
	H	T	S	K	L	E	D	F	T	D	L	L	N	L	T	T	Y	G	F	R	
301	CAT	ACT	TCT	AAA	TTA	GAG	GAT	TTC	ACA	GAT	CTT	TTG	AAT	TTG	ACT	ACT	TAT	GGT	TTT	AGA	
	G	E	A	L	S	S	L	C	A	L	G	N	L	T	V	E	T	R	T	K	
361	GGA	GAA	GCC	TTG	AGC	TCT	CTC	TGT	GCA	TTG	GGA	AAT	CTC	ACT	GGT	GAA	ACA	AGA	ACA	AAG	
	N	E	P	V	A	T	L	L	T	F	D	H	S	G	L	L	T	A	E	K	
421	AAT	GAG	CCA	GTT	GCT	ACG	CTC	TTG	ACG	TTT	GAT	CAT	TCT	GGT	TTG	CTT	ACT	GCT	GAA	AAG	
	K	T	A	R	Q	I	G	T	T	V	T	V	R	K	L	F	S	N	L	P	
481	AAG	ACT	GCT	CGC	CAA	ATT	GGT	ACC	ACT	GTC	ACT	GTT	AGG	AAG	TTG	TTC	TCT	AAT	TTA	CCT	
	V	R	S	K	E	F	K	R	N	I	R	K	E	Y	G	K	L	V	S	L	
541	GTA	CGA	AGC	AAA	GAG	TTT	AAG	CGG	ATT	ATA	CGC	AAA	GAA	TAT	GGG	AAG	CTT	GTA	TCT	TTA	
	L	N	A	Y	A	L	I	A	K	G	V	R	F	V	C	S	N	T	T	G	
601	TTG	AAC	GCA	TAT	TGC	CTT	ATT	CGC	AAA	GGG	GTC	CGG	TTT	GTC	TGC	TCT	AAC	ACG	ACT	GGG	
	K	N	P	K	S	V	V	L	N	T	Q	G	R	G	S	L	K	D	N	I	
661	AAA	AAC	CCA	AAG	TCT	GTT	GTG	CTG	AAC	ACA	CAA	GGG	AGG	GGT	TCA	CTT	AAA	GAT	AAT	ATC	
	I	T	V	F	G	I	S	T	F	T	S	L	Q	P	G	T	G	R	N	L	
721	ATA	ACA	GTT	TTC	GCC	ATT	AGT	ACC	TTT	ACA	AGT	CTA	CAG	CCT	GTC	ACT	GGA	CGC	AAT	TTA	
	A	D	R	Q	Y	F	F	I	N	G	R	P	V	D	M	P	K	V	S	K	
781	GCA	GAT	CGA	CAG	TAT	TTC	TTT	ATA	AAT	GGT	CGG	CCT	GTA	GAT	ATG	CCA	AAA	GTC	AGC	AAG	
	L	V	N	E	L	Y	K	D	T	S	S	R	K	Y	P	V	T	I	L	D	
841	TTG	GTG	AAT	GAG	TTA	TAT	AAA	GAT	ACA	AGT	TCT	CGG	AAA	TAT	CCA	GTT	ACC	ATT	CTG	GAT	
	F	I	V	P	G	G	A	C	D	L	N	V	T	P	D	K	R	K	V	F	
901	TTT	ATT	GTG	CCT	GGT	GGA	GCA	TGT	GAT	TTG	AAT	GTC	ACG	CCC	GAT	AAA	AGA	AAG	GTG	TTC	
	F	S	D	E	T	S	V	I	G	S	L	R	E	G	L	N	E	I	Y	S	
961	TTT	TCT	GAC	GAG	ACT	TCT	GTT	ATC	GGT	TCT	TTG	AGG	GAA	GGT	TG	AAC	GAG	ATA	TAT	TCC	
	S	S	N	A	S	Y	I	V	N	R	F	E	E	N	S	E	Q	P	D	K	
1021	TCC	AGT	AAT	GCG	TCT	TAT	ATT	GTT	AAT	AGG	TTC	GAG	GAG	AAT	TCG	GAG	CAA	CCA	GAT	AAG	
	A	G	V	S	S	F	Q	K	K	S	N	L	L	S	E	G	I	V	L	D	
1081	GCT	GGA	GTT	TCG	TCG	TTT	CAG	AAG	AAA	TCA	AAT	CTT	TTG	TCA	GAA	GGG	ATA	GTT	CTG	GAT	
	V	S	S	K	T	R	L	G	E	A	I	E	K	E	N	P	S	L	R	E	
1141	GTC	AGT	TCT	AAA	ACA	AGA	CTA	GGG	GAA	GCT	ATT	GAG	AAA	GAA	AAT	CCA	TCC	TTA	AGG	GAG	
	V	E	I	D	N	S	S	P	M	E	K	F	K	F	E	I	K	A	C	G	
1201	GTT	GAA	ATT	GAT	AAT	AGT	TCG	CCA	ATG	GAG	AAAG	TTT	AAG	TTT	GAG	ATC	AAG	GCA	TGT	GGG	
	T	K	K	G	E	S	L	S	V	H	D	V	T	H	L	D	K	T	P		
1261	ACG	AAG	AAA	GGG	GAA	GGT	TCT	TTA	TCA	GTC	CAT	GAT	GTA	ACT	CAC	CTT	GAC	AAG	ACA	CCT	
	S	K	G	L	P	Q	L	N	V	T	E	K	V	T	D	A	S	K	D	L	
1321	AGC	AAA	GGT	TTG	CCT	CAG	TTA	AAT	GTG	ACT	GAG	AAA	GTT	ACT	GAT	GCA	AGT	AAA	GAC	TTG	
	S	S	R	S	F	A	Q	S	T	L	N	T	F	V	T	M	G	K	R		
1381	AGC	AGC	CGC	TCT	AGC	TTT	GCC	CAG	TCA	ACT	TTG	AAT	ACT	TTT	GTT	ACC	ATG	GGA	AAA	AGA	
	K	H	E	N	I	S	T	I	L	S	E	T	P	V	L	R	N	Q	T	S	
1441	AAA	CAT	GAA	AAC	ATA	AGC	ACC	ATC	CTC	TCT	GAA	ACA	CCT	GTC	CTC	AGA	AAC	CAA	ACT	TCT	
	S	Y	R	V	E	K	S	K	F	E	V	R	A	L	A	S	R	C	L	V	
1501	AGT	TAT	CGT	GTG	GAG	AAA	AGC	AAA	TTT	GAA	GTT	CGT	GCC	TTA	GCT	TCA	AGG	TGT	CTC	GTG	
	E	G	D	Q	L	D	M	V	I	S	K	E	D	M	T	P	S	E	R		
1561	GAA	GGC	GAT	CAA	CTT	GAT	GAT	ATG	GTC	ATC	TCA	AAG	GAA	GAT	ATG	ACA	CCA	AGC	GAA	AGA	
	D	S	E	L	G	N	R	I	S	P	G	T	Q	A	D	N	V	E	R	H	
1621	GAT	TCT	GAA	CTA	GGC	AAT	CGG	ATT	TCT	CCT	GGA	ACA	CAA	GCT	GAT	ATA	GTT	GAA	AGA	CAT	
	E	R	V	L	G	Q	F	N	L	G	F	I	I	A	K	L	E	R	D	L	
1681	GAG	AGA	GTA	CTC	GGG	CAA	TTC	ATT	CTT	GGG	TTC	ATC	ATT	GCA	AAA	TTG	GAG	CGA	GAT	CTG	
	F	I	V	D	Q	H	A	A	D	E	K	F	N	F	E	H	L	A	R	S	
1741	TTC	ATT	GTG	GAT	CAG	CAT	GCA	GCT	GAT	GAG	AAA	TTC	AAC	TCT	GCA	GAA	CAT	TTC	GCA	AGG	TCA
	T	V	L	N	Q	Q	P	L	L	Q	P	L	N	L	E	L	S	P	E	E	
1801	ACT	GTC	CTG	AC	CAG	CAA	CCC	TTA	CTC	CAG	CCT	TTG	AAC	TTG	GAA	CTC	TCT	CCA	GAA	GAA	
	E	V	T	V	L	M	H	M	D	I	R	E	N	G	F	L	L	E	E		
1861	GAA	GTA	ACT	GTG	TTA	ATG	CAC	ATG	GAT	ATT	ATC	AGG	GAA	AAT	GGC	TTT	CTT	CTA	GAG	GAG	
	N	P	S	A	P	P	G	K	H	F	R	L	R	A	I	P	Y	S	K	N	
1921	AAT	CCA	AGT	GCT	CCT	CCC	GGA	AAA	CAC	TTT	AGA	CTA	CAG	GCC	ATT	CCT	TAT	AGC	AAG	AAT	
	I	T	F	G	V	E	D	L	K	D	L	I	S	T	L	G	D	N	H	G	
1981	ATC	ACC	TTT	GGA	GTC	GAA	GAT	CTT	AAA	GAC	CTG	ATC	TCA	ACT	TCA	GGA	GAT	AAC	CAT	GGG	
	E	C	S	V	A	S	S	Y	K	T	S	K	T	D	S	I	C	P	S	R	
2041	GAA	TGT	TCG	GTT	GCT	AGT	AGC	TAC	AAA	ACC	AGC	AAA	ACA	GAT	TCG	ATT	TGT	CCA	TCA	CGA	
	V	R	A	M	L	A	S	R	A	C	R	S	S	V	M	I	G	D	P	L	
2101	GTC	CGT	GCA	ATG	CTA	GCA	TCC	CGA	GCA	TGC	AGA	TCA	TCT	GTC	ATG	ATC	GGA	GAT	CCA	CTC	
	R	K	N	E	M	Q	K	I	V	E	H	L	A	D	L	E	S	P	W	N	
2161	AGA	AAA	AAC	GAA	ATG	CAG	AAG	ATA	GTA	GAA	CAC	TTG	GCA	GAT	CTC	GAA	TCT	CCT	TGG	AAT	
	C	P	H	G	R	P	T	M	R	H	L	V	D	L	T	T	L	L	T	L	
2221	TGC	CCA	CAC	GGA	GCA	CCA	ACA	ATG	CGT	CAT	CTT	GTC	GAC	TTG	GAA	CTG	ACA	ACT	TTA	CTC	ACA
	P	D	D	D	N	V	N	D	D	D	D	D	D	A	T	I	S	L	A	*	

2281 CCT GAT GAC GAC AAT GTC AAT GAT GAT GAT GAT GAT GAT GCA ACC ATC TCA TTG GCA TGA

Sequence ID 4. *Arabidopsis thaliana* PMS2 homologue (ACCESSION AF069298) cDNA and amino acid sequenc.

M E R A E S S S T E P A K A I K P I D R
1 ATG GAG CGA GCT GAG AGC TCG AGT ACA GAA CCT GCT AAG GCC ATC AAA CCT ATT GAT CCG
K S V H Q I C S G Q V V L S L S T A V K
61 AAG TCA GTC CAT CAG ATT TGC TCT GGG CAG CTG GTA CTG AGT CTA AGC ACT GCG GTA AAG
E L V E N S L D A G A T N I D L K L K D
121 GAG TTA GTA GAA AAC AGT CTG GAT GCT GGT GCC ACT AAT ATT GAT CTA AAG CTT AAG GAC
Y G V D L I E V S D N G C G V E E E N F
181 TAT GGA GTG GAT CTT ATT GAA GTT TCA GAC AAT GGA TGT GGG GTA GAA GAA AAC AAC TTC
E G L T L K H H T S K I Q E F A D L T Q
241 GAA GGC TTA ACT CTG AAA CAT CAC ACA TCT AAG ATT CAA GAG TTT GCC GAC CTA ACT CAG
V E T F G F R G E A L S S L C A L S D V
301 GTT GAA ACT TTT GGC TTT CGG GGG GAA GCT CTG AGC TCA CTT TGT GCA CTG AGC GAT GTC
T I S T C H A S A K V G T *
361 ACC ATT TCT ACC TGC CAC GCA TCG GCG AAG GTT GGA ACT TAG

Sequene ID 5. Human PMS134 cDNA and amino acid sequences.

003321 • 003322 • 003323 • 003324 • 003325

	M	Q	G	D	S	S	P	S	P	T	T	T	S	S	P	L	I	R	P	I
1	ATG	CAA	GGA	GAT	TCT	TCT	CCG	TCT	CCG	ACG	ACT	ACT	AGC	TCT	CCT	TTG	ATA	AGA	CCT	ATA
	N	R	N	V	I	H	R	I	C	S	G	Q	V	I	L	D	L	S	S	A
61	AAC	AGA	AAC	GTA	ATT	CAC	AGA	ATC	TGT	TCC	GGT	CAA	GTC	ATC	TTA	GAC	CTC	TCT	TCG	GCC
	V	K	E	L	V	E	N	S	L	D	A	G	A	T	S	I	E	I	N	L
121	GTC	AAG	GAG	CTT	GTC	GAG	AAT	AGT	CTC	GAC	GCC	GGC	GCC	ACC	AGT	ATA	GAG	ATT	AAC	CTC
	R	D	Y	G	E	D	Y	F	Q	V	I	D	N	G	C	G	I	S	P	T
181	CGA	GAC	TAC	GCC	GAA	GAC	TAT	TTT	CAG	GTC	ATT	GAC	AAT	GGT	TGT	GGC	ATT	TCC	CCA	ACC
	N	F	K	V	C	V	Q	I	L	R	R	T	F	D	V	L	A	L	K	H
241	AAT	TTC	AAG	GTT	TGT	GTC	CAA	ATT	CTC	CGA	AGA	ACT	TTT	GAT	GTT	CTT	GCA	CTT	AAG	CAT
	H	T	S	K	L	E	D	F	T	D	L	L	N	L	T	T	Y	G	F	R
301	CAT	ACT	TCT	AAA	TTA	GAG	GAT	TTC	ACA	GAT	CTT	TTG	AAT	TTG	ACT	ACT	TAT	GGT	TTT	AGA
	G	E	A	L	S	S	L	C	A	L	G	N	L	T	V	E	T	R	T	K
361	GGA	GAA	GCC	TTG	AGC	TCT	CTC	TGT	GCA	TTG	GGA	AAT	CTC	ACT	GTG	GAA	ACA	AGA	ACA	AAG
	N	E	P	V	A	T	L	*												
421	AAT	GAG	CCA	GTT	GCT	ACG	CTC	...												

Sequence ID 6. *Arabidopsis thaliana* PMS134 homologue cDNA and amino acid sequences.

humPMS2	AtPMS2	Consensus	1	70
	(1)	ATGCAGCAGCTGAGAGCTCCACACAGAACCTGCTAGGCC	-	-
	(1)	ATGCAAGGAACTCTTCCTCCGTCGGACGACTACTAGCTCTCTTGATAGACCTATAACAGAAACG	-	-
humPMS2	AtPMS2	Consensus	71	140
	(1)	ATG A GAG T	CG T C	CT CTA C
	(65)	CAGTCATCAGATTCCTCTGGAGCTGACTGAGCTAAGCACTGGGTAAAGGACTTGTAGAAAAA	-	-
humPMS2	AtPMS2	Consensus	(71)	71
	(71)	TAATTCACAGAAATCTCTCCGCAACATCTAGACCTCTGGGCTCAAGGACGCTGCGAGAA	-	-
	(141)	AT T CA AT TG TC GG CA GT T T CT C GC GT AAGGAG T GT GA AA	-	-
humPMS2	AtPMS2	Consensus	141	210
	(135)	CAGTCTGGATGGTGGGCCACTATATTGATCTAACTTAAGGACTATGGAGTGGATCTATTGAGTT	-	-
	(141)	TAGTCCTGACGCCGGCGGCCACCGTATAAGAGATAACCCGAGACTACGGCGAAGACTATTTCAGGTC	-	-
	(141)	AGTCT GA GC GG GCCAC A TAT GA T AA CT GACTA GG G GA T TT A GT	-	-
humPMS2	AtPMS2	Consensus	211	280
	(205)	TCAAGACAATGGATGTGGGT	-	-
humPMS2	AtPMS2	Consensus	(211)	(211)
	(211)	ATTGACAATGGTTGTGECATTTCCTCCAACCAATTTCAGGTTGTGTCCTAACCTCCGAGAATTTC	-	-
	(211)	GACAATGG TGTGG T A AAG AA CT CGAAG	-	-
humPMS2	AtPMS2	Consensus	281	350
	(246)	CTTAACCTCTGAAACATCACACATCTAAAGATTCAGAGTTCCGACCTAACCTAGGGTGAA-ACCT	-	-
humPMS2	AtPMS2	Consensus	(281)	(281)
	(281)	ATGTTCTTGCACTTAAGCATCATCTTCTAAATTAGGGATTTACAGATCTT-IGATETGACTACT	-	-
	T CT CT AA CATCA AC TCTAA T A GA TT C GA CT T A TTGA ACTT	-	-	
humPMS2	AtPMS2	Consensus	351	420
	(311)	TTGGCTTCCGGGGAACCTCTAGCTCACTTGTGCACTGACCCATGTCAACATTCTACTC	-	-
humPMS2	AtPMS2	Consensus	(350)	(350)
	(350)	ATGGTTTAAAGAGAAGCTTGTGCTCTCTGTGCAATTGGAAATCTCACTGTGGAAGAACACAA	-	-
	(351)	TGG TTT G GG GAAC TGAGCTC CT TGTGCA TG G AT TCAC T AC G C A	-	-
humPMS2	AtPMS2	Consensus	421	490
	(379)	GAATCGGGCAGGTTGCAACTGACTGATGTTGATCAAATGGAAAAATA-TCCAGAAAACCCCTAC	-	-
humPMS2	AtPMS2	Consensus	(420)	(420)
	(420)	GAATGASCAA-GTTGCTAACGCTCTGACCTTGATCATTCCTGGTTGTTGTTACTGCTGAAAGACTG	-	-
	(421)	G AT GC A GTT AC C TGA CTTTGATCA TGG TTA T C GAAA	-	-
humPMS2	AtPMS2	Consensus	491	560
	(448)	CCCGCCCGAGGGACCAAGTCAGCTGGCAGACTTATTTGACACTACCTGTGCCCATAGGAA	-	-
humPMS2	AtPMS2	Consensus	(488)	(488)
	(488)	CTCSCCAAATTGGTACCACTGTCACTTTAGGAAGTTGTTCTAATTACCTGTACCAAGCAAGAG	-	-
	(491)	C C GCC A GG ACCAC GTCA GT G AGTT TT TC A TACCTGT CG AA GA T	-	-
humPMS2	AtPMS2	Consensus	561	630
	(518)	TTCAAGGAATAATTAGAAGGATATGCCAAATGGTCCAGGCTTACATGCATACTGTA-CATTTCAGC	-	-
humPMS2	AtPMS2	Consensus	(557)	(557)
	(557)	TTAAGCGGAATAATACGCAAGAAATGGGAAGCTGTTATCTTAAFTGAAACGCTATGCCATTATTGGAA	-	-
	(561)	TT A GGAATAT AA GA TATG AA T GT T TT A GCATA T ATT C	-	-
humPMS2	AtPMS2	Consensus	631	700
	(588)	AGGCATCCGCTTAAGTGGACCCCTCACCTTGGACAAAGGAAACACAGCCGTGGTATGCCACAGGTGGA	-	-
humPMS2	AtPMS2	Consensus	(627)	(627)
	(627)	AGCAGTGGCTTGTGCTGGCTCACGACTGGGAAA-AACCGAAACTCTGTTGT	-	-
	(631)	AGG T CG T TGC C AA G TGG AA AA C A AG CTGT GT G GA	-	-
humPMS2	AtPMS2	Consensus	701	770
	(658)	AGCCCCAGCATAAACCAAATATGGCTCTGTGTTGGCAGAAGCAGTTGCAAAGCCTCATTCTTTG	-	-
humPMS2	AtPMS2	Consensus	(686)	(686)
	(686)	A-C-A-CACAA-GCC-	-	-
	(701)	A CA CA AA GG A G G G	-	-
humPMS2	AtPMS2	Consensus	771	840
	(728)	TTCTAGCTGCCCTAGTCACCTCCCTGTGCAAGAGTACCGTTGAGCTGTTGGATGCGCTGATATCT	-	-
humPMS2	AtPMS2	Consensus	(702)	(702)
	(702)	TTCA-C-T-TAAAGA-TAA-ATCATAAACAGTT	-	-
	(771)	TTCA C TA GA T A A AC GTTT TC GCAT A	-	-
humPMS2	AtPMS2	Consensus	841	910
	(798)	TTTATACATCTAGGTTTCAATTCAACATGCCAGCATGGAGTTGGAAAGGAGTTAACAGACAGACT	-	-
humPMS2	AtPMS2	Consensus	(743)	(743)
	(743)	CTTTTACAAGTC-TACA-GCCTGCTACTGGACGCAATTAGCAGTCAGACAGT	-	-
	(841)	TTTACA TC T CA GC TGG TGG G A TT A CAGA GACAGT T	-	-
humPMS2	AtPMS2	Consensus	911	980
	(868)	TTCTTTATCAACCGCGGGCTTGTGACCCAGCAAAGGTGTCAGACTCGTGAATGGGCTACCGCTG	-	-
humPMS2	AtPMS2	Consensus	(796)	(796)
	(796)	TTCTTTATAATGCTGGGGCTGTGAGATATGCCAAAATGCAAGTGGTGAATGACTAT-AGAGA	-	-
	(911)	TTCTTTAT AA G CGGCCT GA CAAA GTC GCA T GTGAATGAG T TA A A T	-	-
humPMS2	AtPMS2	Consensus	981	1050
	(938)	ATAA-TCCACACCACTATCCATTGTTCTTAACATTTCTGTTGATTCACATTCGGTGAATCAATGATG	-	-
humPMS2	AtPMS2	Consensus	(865)	(865)
	(865)	AAACATCTCGGAAATATCCAGTACCAATTCTGGATTATTTGCTGGTGGTCAAGCAGTCAGATG	-	-
	(981)	A AA T C A TATCCA TT TTCT A TT TGT T G A TGAT T AATG	-	-
humPMS2	AtPMS2	Consensus	1051	1120
	(1007)	TTACTCCAGATAAAACGAAATTGCTACAAAGGAAAGCTTGTGGAGCTTTAAAGACCTCTT	-	-
humPMS2	AtPMS2	Consensus	(935)	(935)
	(935)	TOACCCCCGATAAAAAGAAAGGTTCTTCTGAGGAACTT	-	-
	(1051)	T AC CC GATAAAAG A T TT T T GA GA A CTT TGTT C GTT CTTT	-	-
humPMS2	AtPMS2	Consensus	1121	1190
	(1077)	GATAAGGAATGTTGATAGTGTGCAACACACTAAATGTCAGTCAGCAGAGCCACTGCTGCAAGTGAAGGT	-	-
humPMS2	AtPMS2	Consensus	(993)	(993)
	(993)	GAG-CGAAAGGTGTCGA-A-CGACATATATTCG-T-C-CCAGTAAATGCCCTTATATA	-	-
	(1121)	GA GGAA GT TGA A C AG TA AT C T CCA T TG T TT A	-	-
humPMS2	AtPMS2	Consensus	1191	1260
	(1147)	AACTTAATAAAATGCCATCAGCGCATTGGAAAGGCCATGGTAGAAAGCAGGATCACTCCCTTCT	-	-
humPMS2	AtPMS2	Consensus	(1040)	(1040)
	(1040)	TTGTTAAAGGTTCAAGGAGAAATTGGAGAACCTGAGGAGAACCTGAGAAGGAGTGGTGTGTTGCTG	-	-
	(1191)	T T AA A G G G G ATT GGA A CC AGA AAG G T A C TC T	-	-
humPMS2	AtPMS2	Consensus	1261	1330
	(1217)	TAAGGACTGGAGAAGAAAAAGACGTGTCATTCTAGACTGGAGGAGGCCCTTCTCTGTCACAC	-	-
humPMS2	AtPMS2	Consensus	(1097)	(1097)
	(1097)	ITC-AGAAGAAATCAAATCTTTTGTCAGAA-CGATACAGTAC-TCCTGAGATGTCAGTT	-	-

Consensus	(1261)	T	AGAAGAAA	AAA	TC	TT	CA	GA	G	GA	AG	TTCT	GTCA
	1331												1400
humPMS2	(1287)	AA	CAGA	ACA	AC	CT	CA	CA	CC	AA	AG	ACT	CGA
AtPMS2	(1148)	CTAA	---	AA	CA	AC	CT	AC	GG	AA	GT	CT	AG
Consensus	(1331)	A	AA	CA	AG	CT	AG	AA	T	AG	AA	AA	CC
	1401												1470
humPMS2	(1357)	AT	GCT	C	T	T	CA	GG	CT	TC	GA	AC	TC
AtPMS2	(1212)	TA	AT	AT	CG	CC	AT	GG	GAG	TT	GA	AT	GG
Consensus	(1401)	GT	C	A	AG	T	T	GA	AAG	CT	TG	GAC	AGAAAG
	1471												1540
humPMS2	(1427)	GT	TC	CA	GG	AC	CC	AG	GG	AG	GA	AC	CT
AtPMS2	(1277)	GT	TCT	TT	AT	CA	GT	CT	AT	GT	AA	CT	AC
Consensus	(1471)	GT	T	A	CA	GT	CC	GA	AC	A	T	GA	AAG
	1541												1610
humPMS2	(1497)	T	TG	CG	GG	AT	TT	GG	TT	CAG	AT	CC	AG
AtPMS2	(1334)	C	CA	TT	AA	AA	GT	AC	TT	CA	CC	AC	AG
Consensus	(1541)	TC	GT	A	T	TGA	G	AGA	AGT	ACT	GCA	AGTA	A
	1611												1680
humPMS2	(1567)	TC	CC	AC	GG	GG	AC	GG	GG	CT	GA	AA	CT
AtPMS2	(1376)	ACT	TG	AC	GG	CT	CT	AT	GG	AA	AG	CG	CT
Consensus	(1611)	C	AG	CAG	GCTC	A	T	TG	C	TCA	CT	TGA	ACT
	1681												1750
humPMS2	(1637)	TT	TCA	GT	GG	AC	GT	CC	AT	TC	AG	AA	CT
AtPMS2	(1423)	CT	TAC	AT	GG	-----	AA	AA	AA	AA	AA	AA	AA
Consensus	(1681)	TT	ATG	G	AAA	AAGA	AC	ATG	AAA	C	T	AGC	AC
	1751												1820
humPMS2	(1707)	TA	AT	CT	GG	AA	CC	CC	GG	AT	TT	CG	AG
AtPMS2	(1461)	CA	TCT	CT	GT	-----	AA	AC	CT	CC	TT	TA	TT
Consensus	(1751)	A	CTC	C	AAACAC	GT	T	A	AA	TTCT	AGTT	T	CT
	1821												1890
humPMS2	(1777)	AA	GT	AG	AA	AA	TT	CT	TC	AG	CT	GA	CA
AtPMS2	(1517)	AA	--	AG	AA	AA	TT	GA	AG	TC	TC	AA	AC
Consensus	(1821)	AA	AG	AAAT	AG	C	TG	CT	AG	TT	A	AG	TG
	1891												1960
humPMS2	(1847)	TG	CC	CT	GG	AC	TT	TCT	AT	AG	CT	CA	AG
AtPMS2	(1568)	AT	CA	CT	GT	-----	TT	AT	GT	AT	TC	AA	AC
Consensus	(1891)	C	CT	GA	T	TAT	G	T	A	CT	AA	AG	AAAG
	1961												2030
humPMS2	(1917)	TG	AA	GG	GG	AA	CA	GA	AA	TT	TC	CT	GG
AtPMS2	(1620)	AG	AT	CT	GA	ACT	-----	AG	GA	AA	CC	AA	GG
Consensus	(1961)	GA	GAAC	AG	A	T	G	GATT	TCT	TGGA	A	CAAGC	G
	2031												2100
humPMS2	(1987)	GA	ACT	TA	AG	AA	AG	AA	TT	GA	AA	AT	GG
AtPMS2	(1672)	GA	--	AG	AC	AT	GAGA	G	-----	CG	GG	CA	TT
Consensus	(2031)	GAA	AGA	A	GAGA	A	GTA	C	T	GG	CA	TT	AA
	2101												2170
humPMS2	(2057)	TT	ATA	AA	CC	AA	AA	CT	GA	AT	GG	AA	GT
AtPMS2	(1712)	TC	AT	TT	GG	AA	AA	TT	CT	TC	GG	AA	AA
Consensus	(2101)	T	AT	AT	C	AAA	TG	A	GAT	T	TT	CAT	GT
	2171												2240
humPMS2	(2127)	CG	AG	-	AT	GT	CG	AC	GC	AG	CT	TC	CA
AtPMS2	(1782)	CG	AC	AT	TT	AG	CA	GG	TC	AT	GC	AA	CT
Consensus	(2171)	CGA	AT	GCA	CA	AC	GT	CT	A	GCA	A	CT	A
	2241												2310
humPMS2	(2195)	CT	GT	CT	TT	AA	TA	GA	AC	AA	TT	GG	CT
AtPMS2	(1850)	CT	CC	AC	AA	GA	AA	GA	AA	TT	TC	TT	GT
Consensus	(2241)	CT	C	G	A	GAAG	T	TG	TA	A	TGGA	AT	GG
	2311												2380
humPMS2	(2265)	CG	AT	AA	AA	AT	GCT	CC	AG	CT	AA	AA	AC
AtPMS2	(1920)	GA	AT	CC	AA	CT	G	TCT	GA	CC	AC	AT	AC
Consensus	(2311)	AT	AA	TG	CT	TC	C	GA	AA	CT	CC	GA	T
	2381												2450
humPMS2	(2333)	TG	GG	AC	CC	AA	GG	CC	TG	GG	AC	CC	GG
AtPMS2	(1988)	TG	GG	AT	CA	GA	AA	GT	AT	GG	AA	AT	GG
Consensus	(2381)	T	GG	A	C	GA	T	A	GA	CT	G	GA	AC
	2451												2520
humPMS2	(2398)	-----	-----	-----	-----	-----	-----	-----	-----	CCT	TG	CC	AG
AtPMS2	(2058)	TAG	T	AC	AA	AA	CC	AG	AT	CG	AG	TG	GT
Consensus	(2451)	-----	-----	-----	-----	-----	-----	-----	-----	CC	TC	CG	AG
	2521									AT	G	T	GC
humPMS2	(2434)	TG	GG	GA	AG	TC	GG	GT	AT	GG	AC	CC	AG
AtPMS2	(2128)	TG	GG	AG	AT	CA	TC	GT	GT	AT	GG	AC	AT
Consensus	(2521)	T	GC	G	TC	GT	GAT	GG	T	C	CT	A	AA
	2591												2660
humPMS2	(2504)	GG	CA	GA	TG	CC	AC	CC	CT	GG	AC	CC	GG
AtPMS2	(2198)	CA	GA	TG	CA	AT	CT	CT	GG	AA	AT	GG	AC
Consensus	(2591)	GA	T	GA	CC	TG	AA	TG	CC	CA	GA	T	AC